



results of **BLAST**

BLASTP 2.2.6 [Apr-09-2003]

RID: 1064601845-5875-417649.BLASTQ3

Query=

(89 letters)

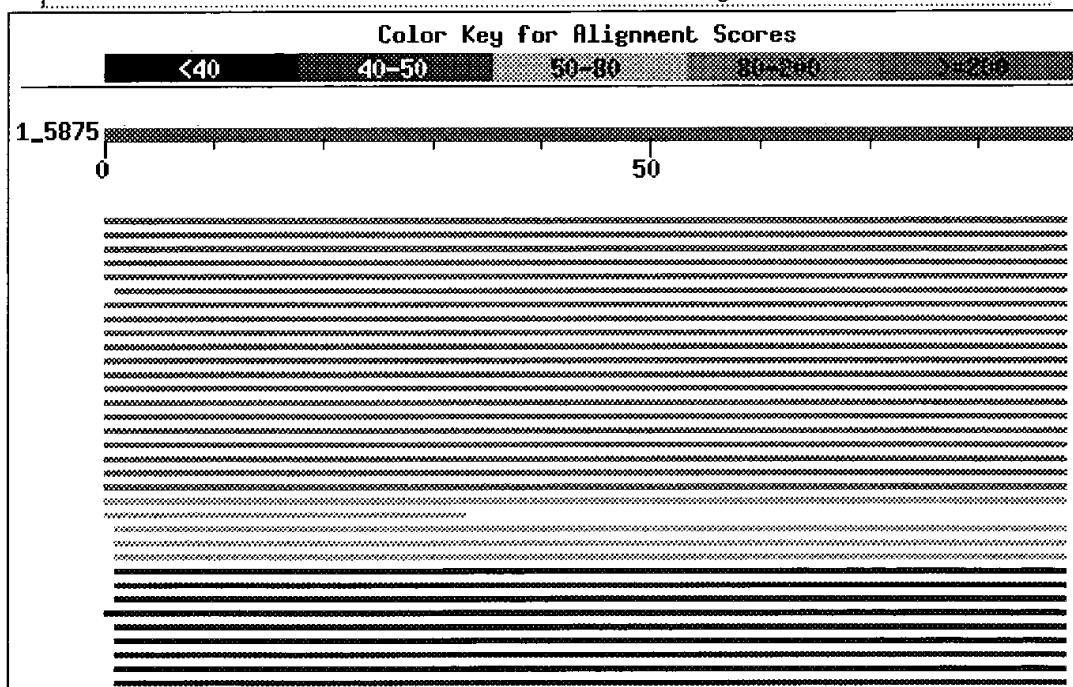
Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

1,538,680 sequences; 497,353,198 total letters

[Taxonomy reports](#)

Distribution of 36 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 3342090 gb AAC27510.1 	gastrin\cholecystokinin brain rec...	165	1e-40	
gi 30584635 gb AAP36570.1 	Homo sapiens cholecystokinin B r...	160	4e-39	
gi 28875799 ref NP_795344.1 	cholecystokinin B receptor; CC...	160	4e-39	
gi 1220299 gb AAA91831.1 	cholecystokinin B receptor	159	1e-38	
gi 7690036 gb AAB30766.2 	cholecystokinin B receptor [Homo ...	159	1e-38	
gi 440912 gb AAB28625.1 	cholecystokinin B/gastrin receptor...	134	3e-31	

gi 15911833 gb AAK38351.1 	CCK-B/gastrin receptor variant [...	129	9e-30	
gi 7677460 gb AAF67174.1 AF239668.1	CCK-B/gastrin receptor ...	129	1e-29	
gi 27806271 ref NP_776687.1 	cholecystokinin B receptor; CC...	120	4e-27	
gi 1169841 sp P46627 GASR_RABIT	Gastrin/cholecystokinin typ...	119	1e-26	
gi 26343361 dbj BAC35337.1 	unnamed protein product [Mus mu...	107	4e-23	
gi 7106265 ref NP_031653.1 	cholecystokinin B receptor; CCK...	107	5e-23	
gi 2654390 gb AAB87706.1 	gastrin/CCK-B receptor [Canis fam...	104	3e-22	
gi 232131 sp P30552 GASR_CANFA	Gastrin/cholecystokinin type...	104	3e-22	
gi 399533 sp P30796 GASR_PRANA	Gastrin/cholecystokinin type...	102	2e-21	
gi 1813461 gb AAB41677.1 	gastrin/cholecystokinin-B receptor	101	3e-21	
gi 1813459 gb AAB41676.1 	gastrin/cholecystokinin receptor	100	8e-21	
gi 1813447 gb AAB41629.1 	gastrin/cholecystokinin receptor	98	3e-20	
gi 6978617 ref NP_037297.1 	cholecystokinin B receptor; CCK...	96	1e-19	
gi 1083622 pir S48049	cholecystokinin B receptor - rat (fr...	92	2e-18	
gi 2495001 sp P70031 CCKR_XENLA	Cholecystokinin receptor (C...	62	2e-09	
gi 26333421 dbj BAC30428.1 	unnamed protein product [Mus mu...	52	2e-06	
gi 2495000 sp Q63931 CCKR_CAVPO	Cholecystokinin type A rece...	52	3e-06	
gi 739858 prf I2004206A	cholecystokinin A receptor	51	3e-06	
gi 6978615 ref NP_036820.1 	cholecystokinin A receptor [Rat...	51	4e-06	
gi 1582179 prf I2118221A	cholecystokinin A receptor	50	1e-05	
gi 4502607 ref NP_000721.1 	cholecystokinin A receptor [Hom...	50	1e-05	
gi 2541920 dbj BAA22847.1 	cholecystokinin type-A receptor ...	49	1e-05	
gi 32400155 emb CAD33800.1 	cholecystokinin receptor [Gallu...	47	7e-05	
gi 12836122 dbj BAB23512.1 	unnamed protein product [Mus mu...	46	1e-04	
gi 6753306 ref NP_033957.1 	cholecystokinin A receptor [Mus...	46	1e-04	
gi 18088214 gb AAH20534.1 	cholecystokinin A receptor [Mus ...	46	1e-04	
gi 1083155 pir S50150	gastric CCK-A receptor - rabbit >gi ...	43	0.001	
gi 10719928 sp O97772 CCKR_RABIT	Cholecystokinin type A rec...	42	0.003	

Alignments

Get selected sequences

Select all

Deselect all

>[gi|3342090|gb|AAC27510.1|](#) gastrin\cholecystokinin brain receptor [Homo sapiens]
Length = 396

Score = 165 bits (418), Expect = 1e-40

Identities = 89/91 (97%), Positives = 89/91 (97%), Gaps = 2/91 (2%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 58

RELYLGLRF DSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP

Sbjct: 192 RELYLGLRFDGSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 251

Query: 59 ALELTALTAPGPGSGSRPTQAKLLAKKRVR 89

ALELTALTAPGPGSGSRPTQAKLLAKKRVR

Sbjct: 252 ALELTALTAPGPGSGSRPTQAKLLAKKRVR 282

>[gi|30584635|gb|AAP36570.1|](#) Homo sapiens cholecystokinin B receptor [synthetic c]
Length = 448

Score = 160 bits (406), Expect = 4e-39
Identities = 89/91 (97%), Positives = 89/91 (97%), Gaps = 2/91 (2%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 58
RELYLGLRF DSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP
Sbjct: 243 RELYLGLRFDGSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 302

Query: 59 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
ALELTALTAPGPGSGSRPTQAKLLAKKRVVR
Sbjct: 303 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 333

>gi|28875799|ref|NP_795344.1| cholecystikinin B receptor; CCK2 receptor; gastr
sapiens]

gi|417029|sp|P32239|GASR HUMAN Gastrin/cholecystikinin type B receptor (CCK-B r
gi|476975|pir|A47430 gastrin/cholecystikinin receptor B, short splice form - hum
gi|179998|qb|AAA35660.1| cholecystikinin receptor
gi|306489|qb|AAA35657.1| cholecystikinin-B/gastrin receptor
gi|406076|qb|AAC37528.1| gastrin receptor
gi|436040|dbj|BAA02564.1| cholecystikinin receptor [Homo sapiens]
gi|12653895|qb|AAH00740.1| Cholecystikinin B receptor [Homo sapiens]
gi|28316421|dbj|BAA04759.2| cholecystikinin-B receptor/gastrin receptor [Homo sap
gi|30582417|qb|AAP35435.1| cholecystikinin B receptor [Homo sapiens]
gi|32482023|qb|AAP84364.1| cholecystikinin B receptor [Homo sapiens]
Length = 447

Score = 160 bits (405), Expect = 4e-39
Identities = 89/91 (97%), Positives = 89/91 (97%), Gaps = 2/91 (2%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 58
RELYLGLRF DSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP
Sbjct: 243 RELYLGLRFDGSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 302

Query: 59 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
ALELTALTAPGPGSGSRPTQAKLLAKKRVVR
Sbjct: 303 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 333

>gi|1220299|qb|AAA91831.1| cholecystikinin B receptor
Length = 447

Score = 159 bits (401), Expect = 1e-38
Identities = 88/91 (96%), Positives = 89/91 (97%), Gaps = 2/91 (2%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 58
RELYLGLRF DSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP
Sbjct: 243 RELYLGLRFDGSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 302

Query: 59 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
ALELTALTAPGPGSGSRPTQAKLLAKKRVVR
Sbjct: 303 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 333

>gi|7690036|gb|AAB30766.2| cholecystokinin B receptor [Homo sapiens]
Length = 447

Score = 159 bits (401), Expect = 1e-38
Identities = 88/91 (96%), Positives = 89/91 (97%), Gaps = 2/91 (2%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRP 58
RELYLGLRF DSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVG+DSDGCVQLPRSRP
Sbjct: 243 RELYLGLRFDGSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGKDSGCVQLPRSRP 302

Query: 59 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
ALELTALTAPGPGSGSRPTQAKLLAKKRVVR
Sbjct: 303 ALELTALTAPGPGSGSRPTQAKLLAKKRVVR 333

>gi|440912|gb|AAB28625.1| cholecystokinin B/gastrin receptor, CCKB/gastrin recep
cytoplasmic domain} [human, small cell lung cancer,
Peptide PartialMutant, 90 aa]
gi|440913|gb|AAB28626.1| cholecystokinin B/gastrin receptor, CCKB/gastrin recepto
cytoplasmic domain} [human, Peptide Partial, 90 aa]
Length = 90

Score = 134 bits (337), Expect = 3e-31
Identities = 88/90 (97%), Positives = 88/90 (97%), Gaps = 2/90 (2%)

Query: 2 ELYLGLRF--DSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPA 59
ELYLGLRF DSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPA
Sbjct: 1 ELYLGLRFDGSDSDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPA 60

Query: 60 LELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
LELTALTAPGPGSGSRPTQAKLLAKKRVVR
Sbjct: 61 LELTALTAPGPGSGSRPTQAKLLAKKRVVR 90

>gi|15911833|gb|AAK38351.1| CCK-B/gastrin receptor variant [Homo sapiens]
gi|23451715|gb|AAN32829.1|AF441129_1 cholecystokinin-C receptor [Homo sapiens]
Length = 516

Score = 129 bits (325), Expect = 9e-30
Identities = 63/63 (100%), Positives = 63/63 (100%)

Query: 27 GAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKR 86
GAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKR
Sbjct: 340 GAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKR 399

Query: 87 VVR 89
VVR
Sbjct: 400 VVR 402

Score = 35.4 bits (80), Expect = 0.21
Identities = 27/29 (93%), Positives = 27/29 (93%), Gaps = 2/29 (6%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGLPG 27
RELYLGLRF DSDSDSQSRVRNQGLPG
Sbjct: 243 RELYLGLRFDGSDSDSQSRVRNQGLPG 271

>gi|7677460|gb|AAF67174.1|AF239668.1 CCK-B/gastrin receptor [Homo sapiens]
Length = 516

Score = 129 bits (324), Expect = 1e-29
Identities = 63/63 (100%), Positives = 63/63 (100%)

Query: 27 GAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKR 86
GAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKR
Sbjct: 340 GAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKR 399

Query: 87 VVR 89
VVR
Sbjct: 400 VVR 402

Score = 35.4 bits (80), Expect = 0.21
Identities = 27/29 (93%), Positives = 27/29 (93%), Gaps = 2/29 (6%)

Query: 1 RELYLGLRF--DSDSQSQRVRNQGLPG 27
RELYLGLRF DSDSQSQRVRNQGLPG
Sbjct: 243 RELYLGLRFDGSDSDSQSRVRNQGLPG 271

>gi|27896271|ref|NP_776687.1| cholecystokinin B receptor; CCK2 receptor [Bos t
gi|3023830|sp|P79266|GASR_BOVIN Gastrin/cholecystokinin type B receptor (CCK-B re
gi|1836140|gb|AAB46896.1| cholecystokinin B-gastrin receptor; CCKB-gastrin rece
taurus]
gi|1588667|prf||2209271A cholecystokinin-B/gastrin receptor
Length = 454

Score = 120 bits (302), Expect = 4e-27
Identities = 67/98 (68%), Positives = 72/98 (73%), Gaps = 9/98 (9%)

Query: 1 RELYLGLRFDSDSDSQSRVR-----NQGLPGAVHQNGRCRPETGAVGEDSDGCVQL 53
RELYLGLRFD DSDS+S+ R G G NGRCR ET GED DGCVQL
Sbjct: 243 RELYLGLRFDGSDSDSESQSRVGSQGLPGGTGQGPANGRCRSETRLAGEDGDGCVQL 302

Query: 54 PRSRPALELTALTA--PGPGSGSRPTQAKLLAKKRVR 89
PRSRPALE++ALTA PGPGSG+RP QAKLLAKKRVR
Sbjct: 303 PRSRPALEMSALTAPTGPBGSGTRPAQAKLLAKKRVR 340

>gi|1169841|sp|P46627|GASR_RABIT Gastrin/cholecystokinin type B receptor (CCK-B
gi|1083156|pir||JC2459 gastrin/cholecystokinin B receptor - rabbit
gi|495665|gb|AAA31194.1| gastrin
Length = 452

Score = 119 bits (297), Expect = 1e-26
Identities = 76/98 (77%), Positives = 78/98 (79%), Gaps = 9/98 (9%)

Query: 1 RELYLGLRF--DSDSQSQRVRNQ-----GGLPGAVHQNGRCRPETGAVGEDSDGCVQL 53
RELYLGLRF DSDS+SQSRVR Q G PG VHQNGRCRPE G GED DGCVQL
Sbjct: 241 RELYLGLRFDSDSDSESQSRVRGQGLPGGAAPGPVHNGRCRPEAGLAGEDGDGCVQL 300

Query: 54 PRSRPALELTALTAP--GPGSGSRPTQAKLLAKKRVVR 89
 PRSRPALEL+ALTAP GPG G RP QAKLLAKKRVVR
 Sbjct: 301 PRSRPALELSALTAPISGPGGPRPAQAKLLAKKRVVR 338

>gi|26343361|dbj|BAC35337.1| unnamed protein product [Mus musculus]
 Length = 453

Score = 107 bits (267), Expect = 4e-23
 Identities = 66/97 (68%), Positives = 68/97 (70%), Gaps = 8/97 (8%)

Query: 1 RELYLGLRFDSDSDS--QSRVRNQGGLPGA-----VHQNGRCRPETGAVGEDSDGCVVQ 52
 RELYLGLRFD D+DS QSRVRNQGGLPG VHONG CR T GEDSDGCVVQ
 Sbjct: 243 RELYLGLRFDGDNDSETQSRVRNQGGLPGGAAAPGPVHQNGGCRHVTSLTGEDSDGCVVQ 302

Query: 53 LPRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
 LPRSR + GPG G RP QAKLLAKKRVVR
 Sbjct: 303 LPRSRLEMTTLTPTTGP GPGPRPNQAKLLAKKRVVR 339

>gi|7106265|ref|NP_031653.1| cholecystokinin B receptor; CCK-B/gastrin recepto
 receptor; CCK2/gastrin [Mus musculus]
 gi|3023828|sp|P56481|GASR_MOUSE Gastrin/cholecystokinin type B receptor (CCK-B
 gi|2460177|gb|AAB71863.1| CCK-B/gastrin receptor [Mus musculus]
 gi|9964011|gb|AAG09801.1| cholecystokinin-B receptor [Mus musculus]
 gi|26390338|dbj|BAC25881.1| unnamed protein product [Mus musculus]
 Length = 453

Score = 107 bits (267), Expect = 5e-23
 Identities = 66/97 (68%), Positives = 68/97 (70%), Gaps = 8/97 (8%)

Query: 1 RELYLGLRFDSDSDS--QSRVRNQGGLPGA-----VHQNGRCRPETGAVGEDSDGCVVQ 52
 RELYLGLRFD D+DS QSRVRNQGGLPG VHONG CR T GEDSDGCVVQ
 Sbjct: 243 RELYLGLRFDGDNDSETQSRVRNQGGLPGGAAAPGPVHQNGGCRHVTSLTGEDSDGCVVQ 302

Query: 53 LPRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
 LPRSR + GPG G RP QAKLLAKKRVVR
 Sbjct: 303 LPRSRLEMTTLTPTTGP GPGPRPNQAKLLAKKRVVR 339

>gi|2654390|gb|AAB87706.1| gastrin/CCK-B receptor [Canis familiaris]
 Length = 454

Score = 104 bits (260), Expect = 3e-22
 Identities = 67/96 (69%), Positives = 70/96 (72%), Gaps = 7/96 (7%)

Query: 1 RELYLGLRFDSDSDSQSRVRNQ-----GGLPGAVHQNGRCRPETGAVGEDSDGCVVQLPR 55
 RELYLGLRFD DSDS+SRVR+Q G PG NG CRPE G GED DGCVVQLPR
 Sbjct: 245 RELYLGLRFDSDSDSESVRVRSQGGLRGAGPGPPANGSCRPEGLAGEDGDGCVVQLPR 304

Query: 56 SRPALELTALTAPGPGSGSRPT--QAKLLAKKRVVR 89
 SR LEL+ALTAP PG G P QAKLLAKKRVVR
 Sbjct: 305 SRQTLLELSALTAPTGP GGGPRPYQAKLLAKKRVVR 340

>gi|232131|sp|P30552|GASR_CANFA Gastrin/cholecystokinin type B receptor (CCK-B r
gi|423174|pir||S32817 gastrin receptor - dog
gi|163957|gb|AAA30847.1| gastrin receptor
 Length = 453

Score = 104 bits (260), Expect = 3e-22
 Identities = 67/96 (69%), Positives = 70/96 (72%), Gaps = 7/96 (7%)

Query: 1 RELYLGLRFDSDSDSQSRVRNQ-----GGLPGAVHQNGRCRPETGAVGEDSDGCVQLPR 55
 RELYLGLRFD DSDS+SRVR+Q G PG NG CRPE G GED DGCYVQLPR
 Sbjct: 244 RELYLGLRFDSDSDSESRVRSQGGLRGGAGPGPAPPNGSCRPEGGLAGEDGDGCVQLPR 303

Query: 56 SRPALELTALTAPGPGSGSRPT--QAKLLAKKRVR 89
 SR LEL+ALTAP PG G P QAKLLAKKRVR
 Sbjct: 304 SRQTELSALTAPTGPGGGPRPYQAKLLAKKRVR 339

>gi|399533|sp|P30796|GASR_PRANA Gastrin/cholecystokinin type B receptor (CCK-B r
gi|112583|pir||JQ1614 gastrin receptor - multimammate rat (*Mastomys natalensis*)
gi|220647|dbj|BAA02250.1| gastrin/cholecystokinin-B receptor [*Mastomys natalensis*]
 Length = 450

Score = 102 bits (253), Expect = 2e-21
 Identities = 65/96 (67%), Positives = 69/96 (71%), Gaps = 9/96 (9%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGGLPGA-----VHQNGRCRPETGAVGEDSDGCVQL 53
 RELYLGLRF D+DSD+QSRVRNQGGLPG VHQNG CR T A GED+DGCYVQL
 Sbjct: 243 RELYLGLRFDGNDSDTQSRVRNQGGLPGGTAPGPVHQNGGCRHVTVA-GEDNDGCVQL 301

Query: 54 PRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVR 89
 PRSR + PGPG S QAKLLAKKRVR
 Sbjct: 302 PRSRLEMTTLTPTPGPGLAS-ANQAKLLAKKRVR 336

>gi|1813461|gb|AAB41677.1| gastrin/cholecystokinin-B receptor
 Length = 450

Score = 101 bits (251), Expect = 3e-21
 Identities = 65/96 (67%), Positives = 69/96 (71%), Gaps = 9/96 (9%)

Query: 1 RELYLGLRF--DSDSDSQSRVRNQGGLPGA-----VHQNGRCRPETGAVGEDSDGCVQL 53
 RELYLGLRF D+DSD+QSRVRNQGGLPG VHQNG CR T A GED+DGCYVQL
 Sbjct: 243 RELYLGLRFDGNDSDTQSRVRNQGGLPGGTAPGPVHQNGGCRHVTVA-GEDNDGCVQL 301

Query: 54 PRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVR 89
 PRSR + PGPG S QAKLLAKKRVR
 Sbjct: 302 PRSRLEMTTLTPTPGPGLAS-ANQAKLLAKKRVR 336

>gi|1813459|gb|AAB41676.1| gastrin/cholecystokinin receptor
 Length = 296

Score = 99.8 bits (247), Expect = 8e-21
 Identities = 65/96 (67%), Positives = 69/96 (71%), Gaps = 9/96 (9%)

Query: 1 RELYLGLRF--SDSDSQSRVRNQGGPLGA-----VHQNGRCRPETGAVGEDSDGCVVQL 53
 RELYLGLRF D+DSD+QSRVRNQGGPLG VHQNG CR T A GED+DGCYVQL
 Sbjct: 99 RELYLGLRFDGNDSDTQSRVRNQGGPLGGTAPGPFVHQNGGCRHVTVA-GEDNDGCVVQL 157

Query: 54 PRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
 PRSR + PPG S QAKLLAKKRVVR
 Sbjct: 158 PRSRLEMTTLTPTPGPLAS-ANQAKLLAKKRVVR 192

>gi|1813447|gb|AAB41829.1| gastrin/cholecystokinin receptor
 Length = 316

Score = 97.8 bits (242), Expect = 3e-20
 Identities = 64/96 (66%), Positives = 68/96 (70%), Gaps = 9/96 (9%)

Query: 1 RELYLGLRF--SDSDSQSRVRNQGGPLGA-----VHQNGRCRPETGAVGEDSDGCVVQL 53
 RELYLGLRF D+DSD+QSRVRN GGLPG VHQNG CR T A GED+DGCYVQL
 Sbjct: 111 RELYLGLRFDGNDSDTQSRVRNXGGLPGGTAPGPFVHQNGGCRHVTVA-GEDNDGCVVQL 169

Query: 54 PRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
 PRSR + PPG S QAKLLAKKRVVR
 Sbjct: 170 PRSRLEMTTLTPTPGPLAS-ANQAKLLAKKRVVR 204

>gi|6978617|ref|NP_037297.1| cholecystokinin B receptor; CCK(B) receptor; CCK2
 norvegicus]
 gi|232132|sp|P30553|GASR_RAT Gastrin/cholecystokinin type B receptor (CCK-B recep
 gi|423801|pir|A46195 cholecystokinin B receptor subtype - rat
 gi|203460|gb|AAA40925.1| cholecystokinin receptor
 Length = 452

Score = 95.9 bits (237), Expect = 1e-19
 Identities = 61/96 (63%), Positives = 65/96 (67%), Gaps = 7/96 (7%)

Query: 1 RELYLGLRFD--SDSDSQSRVRNQ-----GGLPGAVHQNGRCRPETGAVGEDSDGCVVQL 53
 RELYLGL FD +DS++QSR RNQ G PG VHQNG CRP T GEDSDGC VQL
 Sbjct: 243 RELYLGLHFDGENDSETQSRARNQGGPLGGGAAPGPFVHQNGGCRPVT SVAGEDSDGCCVQL 302

Query: 54 PRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
 PRSR + PGP G RP QAKLLAKKRVVR
 Sbjct: 303 PRSRLEMTTLTPTPGVPVGP RP NQAKLLAKKRVVR 338

>gi|1083622|pir|S48049 cholecystokinin B receptor - rat (fragment)
 gi|558237|emb|CAA55798.1| CCK(B) receptor [Rattus norvegicus]
 gi|31872397|gb|AAP59041.1| CCK2 receptor [Rattus norvegicus]
 Length = 381

Score = 91.7 bits (226), Expect = 2e-18
 Identities = 61/96 (63%), Positives = 65/96 (67%), Gaps = 7/96 (7%)

Query: 1 RELYLGLRFD--SDSDSQSRVRNQ-----GGLPGAVHQNGRCRPETGAVGEDSDGCVVQL 53
 RELYLGL FD +DS++QSR RNQ G PG VHQNG CRP T GEDSDGC VQL
 Sbjct: 172 RELYLGLHFDGENDSETQSRARNQGGPLGGGAAPGPFVHQNGGCRPVT SVAGEDSDGCCVQL 231

Query: 54 PRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVR 89
PRSR + PGP G RP QAKLLAKKRVVR
Sbjct: 232 PRSRLEMTTLTTPPGVPVGPVPRNQAKLLAKKRVVR 267

>gi|2495001|sp|P70031|CCKR_XENLA Cholecystokinin receptor (CCK-XLR)
gi|1572485|gb|AAB09052.1| cholecystokinin receptor
Length = 453

Score = 62.0 bits (149), Expect = 2e-09
Identities = 32/93 (34%), Positives = 52/93 (55%), Gaps = 14/93 (15%)

Query: 1 RELYLGLRFDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPAL 60
RELY G++F+ D + +++ H+NG P T G++ DGCY+Q+ + R +
Sbjct: 261 RELYRGIQFEMDLNKEAK-----AHKNGVSTPTTIPSGDEGDGCVIQVTKRRNTM 310

Query: 61 ELTALTAPGPGSGSRP----TQAKLLAKKRVVR 89
E++ LT R ++AKL+AKKRV+R
Sbjct: 311 EMSTLTSPSVCTKMDRARINNSEAKLMAKKRVIR 343

>gi|26333421|dbj|BAC30428.1| unnamed protein product [Mus musculus]
Length = 314

Score = 52.0 bits (123), Expect = 2e-06
Identities = 28/39 (71%), Positives = 29/39 (74%), Gaps = 5/39 (12%)

Query: 1 RELYLGLRFDSDSDS--QSRVRNQGGLPGAVHQ---NGR 34
RELYLGLRFD D+DS QSRVRNQGGLP NGR
Sbjct: 243 RELYLGLRFDGNDNDSETQSRVRNQGGLPGGAAAPDFNGR 281

>gi|2495000|sp|Q63931|CCKR_CAVPO Cholecystokinin type A receptor (CCK-A receptor
gi|2147182|pir|I51898 cholecystokinin A receptor - guinea pig
gi|544724|gb|AAB29504.1| cholecystokinin A receptor; CCK-A receptor [Cavia]
Length = 430

Score = 51.6 bits (122), Expect = 3e-06
Identities = 34/96 (35%), Positives = 46/96 (47%), Gaps = 23/96 (23%)

Query: 2 ELYLGLRFDSDSDSQSRVRNQGGLPGAVHQNGRCRPETGAVG--EDSDGCVQLPRSRPA 59
ELY G++FD+ ++ R + TG+ G EDSGCVY+Q R
Sbjct: 235 ELYQGIKFDIAIQKSAKER-----KTSTGSSGPMEDSDGCVLQKSRHPRK 279

Query: 60 LELTALTAPGPGSG-----SRPTQAKLLAKKRVVR 89
LEL L+ GS S + A L+AKKRV+R
Sbjct: 280 LELRQLSPSSSGSNRINRIRSSSSSTANLMAKKRVIR 315

>gi|739858|prf||2004206A cholecystokinin A receptor
Length = 450

Score = 51.2 bits (121), Expect = 3e-06
Identities = 34/96 (35%), Positives = 46/96 (47%), Gaps = 23/96 (23%)

Query: 2 ELYLGLRFDSQSRVRNQGLPGAVHQNGRCRPETGAVG--EDSDGCVQLPRSRPA 59
 ELY G++FD+ ++ R + TG+ G EDSDGCV+Q R
 Sbjct: 255 ELYQGIKFDIAIQKSAKER-----KTSTGSSGPMEDSDGCVLQKSRHPRK 299

Query: 60 LELTALTAPGPGSG-----SRPTQAKLLAKKRVVR 89
 LEL L+ GS S + A L+AKKRV+R
 Sbjct: 300 LELRQLSPSSSGSNRINRIRSSSSSTANLMAKKRVIR 335

>gi|6978615|ref|NP_036820.1| cholecystokinin A receptor [Rattus norvegicus]
 gi|231713|sp|P30551|CCKR_RAT Cholecystokinin type A receptor (CCK-A receptor) (CC
 gi|285238|pir|A42685 cholecystokinin receptor type A - rat
 gi|203384|gb|AAA40899.1| cholecystokinin receptor
 gi|1100753|dbj|BAA09170.1| cholecystokinin type-A receptor [Rattus norvegicus]
 Length = 444

Score = 50.8 bits (120), Expect = 4e-06
 Identities = 33/95 (34%), Positives = 47/95 (49%), Gaps = 22/95 (23%)

Query: 2 ELYLGLRFDSQSRVRNQGLPGAVHQNGRCRPETGAVG--EDSDGCVQLPRSRPA 59
 ELY G++FD+ ++ + +P TG+ EDSDGCV+Q R
 Sbjct: 250 ELYQGIKFDASQKSAKEK-----KPSTGSSTRYEDSDGCVLQKSRPPRK 294

Query: 60 LELTALTAPGPGSG-----GSRPTQAKLLAKKRVVR 89
 LEL L++ GS S + A L+AKKRV+R
 Sbjct: 295 LELQQLSSGSGSRLNRIRSSSSAANLIAKKRVIR 329

>gi|1582179|prf||2118221A cholecystokinin A receptor
 Length = 428

Score = 49.7 bits (117), Expect = 1e-05
 Identities = 34/97 (35%), Positives = 47/97 (48%), Gaps = 27/97 (27%)

Query: 2 ELYLGLRFDSQSRVRNQGLPGAVHQNGRCRPETGAVG--EDSDGCVQLPRSRPA 59
 ELY G++F++ ++ R +P T + G EDSDGCV+Q R
 Sbjct: 235 ELYQGIKFEASQKSAKER-----KPSTTSSGKYEDSDGCVLQKTRPPRK 279

Query: 60 LELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 89
 LEL L+ GS SR + A L+AKKRV+R
 Sbjct: 280 LELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR 313

>gi|4502607|ref|NP_000721.1| cholecystokinin A receptor [Homo sapiens]
 gi|416772|sp|P32238|CCKR_HUMAN Cholecystokinin type A receptor (CCK-A receptor)
 gi|484443|pir|JN0692 cholecystokinin type A receptor - human
 gi|306491|gb|AAA35659.1| cholecystokinin A receptor
 gi|306596|gb|AAA02819.1| cholecystokinin A receptor
 gi|1209500|gb|AAA91123.1| cholecystokinin type A receptor
 gi|7008027|dbj|BAA90879.1| cholecystokinin type-A receptor [Homo sapiens]
 gi|32482019|gb|AAP84362.1| cholecystokinin A receptor [Homo sapiens]
 Length = 428

Score = 49.7 bits (117), Expect = 1e-05
 Identities = 34/97 (35%), Positives = 47/97 (48%), Gaps = 27/97 (27%)

Query: 2 ELYLGLRFDSQSRVRNQGLPGAVHQNGRCRPETGAVG--EDSDGCVQLPRSRPA 59
 ELY G++F++ ++ R +P T + G ESDGCV+Q R
 Sbjct: 235 ELYQGIKFEASQKSAKER-----KPSTTSSGKYEDSDGCVLQKTRPPRK 279

Query: 60 LELTALTAPGPGSGSRPTQ-----AKLLAKKRVVR 89
 LEL L+ GS SR + A L+AKKRV+R
 Sbjct: 280 LELRQLST---GSSSRANRIRSNSSAANLMAKKRVIR 313

>gi|2541920|dbj|BAA22847.1| cholecystokinin type-A receptor [Rattus norvegicus]
 Length = 307

Score = 49.3 bits (116), Expect = 1e-05.
 Identities = 33/95 (34%), Positives = 47/95 (49%), Gaps = 22/95 (23%)

Query: 2 ELYLGLRFDSQSRVRNQGLPGAVHQNGRCRPETGAVG--EDSDGCVQLPRSRPA 59
 ELY G++FD+ ++ + +P TG+ ESDGCV+Q R
 Sbjct: 113 ELYQGIKFDASQKSAKEK-----KPSTGSSTRYEDSDGCVLQKSRPPRK 157

Query: 60 LELTALTAPGPGS-----GSRPTQAKLLAKKRVVR 89
 LEL L++ GS S + A L+AKKRV+R
 Sbjct: 158 LELQLSSGSGSRLNRIRSSSSAANLIAKKRVIR 192

>gi|32400155|emb|CAD33800.1| cholecystokinin receptor [Gallus gallus]
 Length = 436

Score = 47.0 bits (110), Expect = 7e-05
 Identities = 34/93 (36%), Positives = 47/93 (50%), Gaps = 19/93 (20%)

Query: 1 RELYLGLRFDSQSRV-RNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPA 59
 RELY G+RF+ D ++ R+ LP ++ DGCY+QL R A
 Sbjct: 250 RELYRGIRFELDIKGEAAQQRSTEPLPTC-----DEGDGCVLQLSRPGGA 294

Query: 60 LELTALTAPGPGSGS---RPTQAKLLAKKRVVR 89
 LEL AL A G ++AKL+AK+RV+R
 Sbjct: 295 LELRALGAAGAQQERARINSSEAKLVAKRRVIR 327

>gi|12836122|dbj|BAB23512.1| unnamed protein product [Mus musculus]
 Length = 436

Score = 46.2 bits (108), Expect = 1e-04
 Identities = 31/93 (33%), Positives = 43/93 (46%), Gaps = 11/93 (11%)

Query: 2 ELYLGLRFDSQSRVRNQGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALE 61
 ELY G++FD+ ++ + G + R ESDGCV+Q R LE
 Sbjct: 235 ELYQGIKFDASQKSAKEKRLSSGGGGGGSSSSRY-----EDSDGCVLQKSRPPRKLE 288

Query: 62 LTALTAPGPGS-----GSRPTQAKLLAKKRVVR 89
 L L+ G S + A L+AKKRV+R
 Sbjct: 289 LQQLSTSSSGGRINRIRSSGSAANLIAKKRVIR 321

>gi|6753306|ref|NP_033957.1| cholecystokinin A receptor [Mus musculus]
 gi|6225102|sp|O08786|CKKR MOUSE Cholecystokinin type A receptor (CKK-A receptor
 gi|7438588|pir||JC5599 cholecystokinin-A receptor - mouse
 gi|2114152|dbj|BAA20068.1| cholecystokinin type-A receptor [Mus musculus]
 gi|2984512|gb|AAC07949.1| cholecystokinin-A receptor [Mus musculus]

Length = 436

Score = 45.8 bits (107), Expect = 1e-04

Identities = 31/93 (33%), Positives = 43/93 (46%), Gaps = 11/93 (11%)

Query: 2 ELYLGLRFDSQSRVRNQGGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALE 61
 ELY G++FD+ ++ + G + R ESDGCV+Q R LE
 Sbjct: 235 ELYQGIKFDASQKKSAREKRLSSGGGGGGSSSSRY-----EDSDGCVLQKSRPPRKLE 288

Query: 62 LTALTAPGPGS-----GSRPTQAKLLAKKRVVR 89
 L L+ G S + A L+AKKRV+R
 Sbjct: 289 LQQLSTSSSGGRINRIRSSGSAANLIAKKRVIR 321

>gi|18088214|gb|AAH20534.1| cholecystokinin A receptor [Mus musculus]
 Length = 436

Score = 45.8 bits (107), Expect = 1e-04

Identities = 31/93 (33%), Positives = 43/93 (46%), Gaps = 11/93 (11%)

Query: 2 ELYLGLRFDSQSRVRNQGGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPALE 61
 ELY G++FD+ ++ + G + R ESDGCV+Q R LE
 Sbjct: 235 ELYQGIKFDASQKKSAREKRLSSGGGGGGSSSSRY-----EDSDGCVLQKSRPPRKLE 288

Query: 62 LTALTAPGPGS-----GSRPTQAKLLAKKRVVR 89
 L L+ G S + A L+AKKRV+R
 Sbjct: 289 LQQLSTSSSGGRINRIRSSGSAANLIAKKRVIR 321

>gi|1083155|pir||S50150 gastric CCK-A receptor - rabbit
 gi|896235|gb|AAB32223.1| cholecystokinin receptor subtype A, CCK-A receptor=G pro
 coupled receptor [rabbits, fundic epithelium, Peptide,
 427 aa]
 gi|1091571|prf||2021259A cholecystokinin A receptor
 Length = 427

Score = 43.1 bits (100), Expect = 0.001

Identities = 36/94 (38%), Positives = 49/94 (52%), Gaps = 22/94 (23%)

Query: 2 ELYLGLRFDSQSRVRNQGGGLPGAVHQNGRCRPETGAVGEDSDGCVQLPRSRPA-- 59
 ELY G++FD+ ++ R A +GR ED+DGCY+Q RS+P
 Sbjct: 235 ELYQGIKFDASQKKSAREK-----ASTGSGRF-----EDNDGCVLQ--RSKPTRQ 278

Query: 60 LELTALTAPGPGSGSR----PTQAKLLAKKRVVR 89
 LEL L+ G G SR + A L+AKKRV+R
 Sbjct: 279 LELQQLSGGGGGRVSRHSSSSAAALMAKKRVIR 312

☐ >gi|10719928|sp|O97772|CCKR_RABIT Cholecystokinin type A receptor (CCK-A recepto
gi|4205090|gb|AAD11547.1| gastric cholecystokinin A receptor [Oryctolagus cunicul
Length = 427

Score = 41.6 bits (96), Expect = 0.003

Identities = 33/94 (35%), Positives = 46/94 (48%), Gaps = 22/94 (23%)

Query: 2 ELYLGLRFDSQSDSQSRVRNQGGLPQAVHQNGRCRPETGAVGEDSDGCVVQLPRSRPA-- 59

ELY G++FD+ ++ R A +GR ED+DGCY+Q RS+P

Sbjct: 235 ELYQGIKFDASQKSAKERK-----ASTGSGRF-----EDNDGCVLQ--RSKPTRQ 278

Query: 60 LELTALT----APGPGSGSRPTQAKLLAKKRVVR 89

LEL L+ S + A L+AKKRV+R

Sbjct: 279 LELQQLSGGGGGRVSRIRSSSSAATLMAKKRVIR 312

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Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

Posted date: Sep 26, 2003 1:54 AM

Number of letters in database: 497,353,198

Number of sequences in database: 1,538,680

Lambda	K	H
0.314	0.135	0.395

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 24,766,440

Number of Sequences: 1538680

Number of extensions: 1017597

Number of successful extensions: 1602

Number of sequences better than 10.0: 10

Number of HSP's better than 10.0 without gapping: 9

Number of HSP's successfully gapped in prelim test: 3

Number of HSP's that attempted gapping in prelim test: 1576

Number of HSP's gapped (non-prelim): 15

length of query: 89

length of database: 497,353,198

effective HSP length: 65

effective length of query: 24

effective length of database: 397,338,998

effective search space: 9536135952

effective search space used: 9536135952

T: 11

A: 40

X1: 16 (7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 42 (21.9 bits)

S2: 66 (30.0 bits)

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- ☐ 1. *J Biol Chem* 1994, **269** (45):27791-4

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Palmitoylation of G protein-coupled receptor kinase, GRK6. Lipid modification diversity in the GRK family.

Stoffel, R H. , Randall, R R. , Premont, R T. , Lefkowitz, R J. , Inglese, J.

Howard Hughes Medical Institute, Duke University Medical Center, Durham, North Carolina 27710.

GRK6, a 66-kDa serine/threonine protein kinase, is a recently identified member of the G protein-coupled receptor kinase (GRK) family. GRKs are involved in the phosphorylation of seven-transmembrane receptors, a process mediating desensitization of signal transduction. An important feature of these enzymes is their membrane-associated nature, which for some members is stimulus-dependent. The structural basis for this membrane association previously has been shown in different members of the GRK family to include isoprenylation, G protein beta gamma-binding domains, and basic regions to provide electrostatic interactions with phospholipids. We provide evidence that another mechanism includes fatty acid acylation. GRK6, but not other GRKs tested, incorporated tritium after incubation with [3H]palmitate in Sf9 and in COS-7 cells overexpressing the kinase. The incorporated radioactivity was released from the protein by neutral hydroxylamine, indicating the presence of a thioester bond, and was confirmed as palmitic acid by high performance liquid chromatography analysis. Site-directed mutagenesis defined the region of palmitate attachment as a cluster of 3 cysteines (Cys561, Cys562, and Cys565) in the carboxyl-terminal domain of the kinase, consistent with the location of the membrane targeting domains

of GRKs 1, 2, 3, and 5. Palmitoylation of GRK6 appears essential for membrane association, since palmitoylated kinase was found only in the membrane fraction. This lipid modification provides a structural basis for potential regulation of the subcellular distribution of GRK6 through acylation/deacylation cycles.

MedlineID: 95050538

PMID: 7961702

ISSN: 0021-9258

Publication Type:
Journal Article

Substances:

Palmitic Acids

Plasmids

Potassium Channels

delayed rectifier potassium channel

Cysteine

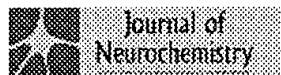
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The metabotropic glutamate receptor mGluR4, but not mGluR1 alpha, is palmitoylated when expressed in BHK cells

S Alaluf, ER Mulvihill and RA McIlhinney

Medical Research Council Anatomical Neuropharmacology Unit, Oxford, England.

Several G protein-coupled receptors have been shown to be palmitoylated, and for some of these receptors the covalent attachment of palmitate has been implicated in the regulation of receptor-G protein coupling. The metabotropic glutamate receptor (mGluR) family forms a distinct group of G protein-coupled receptors, and the possibility that these may also be palmitoylated has been examined. Clonal baby hamster kidney (BHK) cells permanently transfected with the mGluR4 and mGluR1 alpha subtypes were labelled with [3H]palmitic acid. The cells were lysed, the receptors were immunoprecipitated with specific antipeptide antibodies, and the immunoprecipitates were analysed by sodium dodecyl sulphate-polyacrylamide gel electrophoresis and autoradiography. The palmitoylated, endogenously expressed G protein alpha-subunit alpha q could be immunoprecipitated from [3H]palmitate-labelled BHK cells expressing mGluR1 alpha using a specific antipeptide antibody, but in the same cell lysates no detectable [3H]palmitate-labelled mGluR1 alpha was found. This suggests that this mGluR subtype, associated with stimulation of phospholipase C, is not palmitoylated. In contrast, mGluR4, which is coupled to inhibition of adenylyl cyclase, was found to be labelled with [3H]palmitic acid, and the palmitate was quantitatively removed by treatment with 1 M hydroxylamine, suggesting attachment of the palmitate through a thioester bond. Stimulation with maximal doses of the neurotransmitter glutamate for 1, 5, or 10 min appeared to have no effect on the level of receptor palmitoylation.

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